PTO/SB/21 (12-97)
Approved for use through 9/30/00. OMB 0651-0031
Patent and Trademark Office: U.S. Department of Commerce

TRANSMITTAL FORM

(To be used for all correspondence after initial filing)

Application Number	09/786,635
Filing Date	May 22, 2001
First Named Inventor	Gerd Schmitz
Group Art Unit	1646
Examiner Name	Joseph F. Murphy

Total Number of Pages in This Submission		Attorney Docket Number	Bayer 10,131-KGB

TECH CENTER 1600/2900

RECEIVED OCT 09 2002

ENCLOSURES (*check all that apply*)

☐ Fee Transmittal Form
  ☐ Fee Attached

☐ Amendment / Response
  ☐ After Final

☐ Affidavits/declaration(s)

☐ Extension of Time Request

☐ Express Abandonment Request

☐ Information Disclosure Statement

☐ Certified Copy of Priority Document(s)

☐ Response to Missing Parts/ Incomplete Application

  ☐ Response to Missing Parts under 37 CFR 1.52 or 1.53

☐ Assignment Papers *(for an Application)*

☐ Drawing(s)

☐ Licensing-related Papers

☐ Petition

☐ To convert a Provisional Application

☐ Power of Attorney, Revocation Change of Correspondence Address

☐ Terminal Disclaimer

☐ Small Entity Statement

☐ Request for Refund

☐ After Allowance Communication to Group

☐ Appeal Communication to Board of Appeals and Interferences

☐ Appeal Communication to Group *(Appeal Notice, Brief, Reply Brief)*

☐ Proprietary Information

☐ Status Letter

☒ Additional Enclosure(s) -(please identify below):

- Response to Notice; Diskette containing substitute computer readable form (CRF) copy of the Sequence Listing; copy of Notice to Comply with Requirements for Patent Applications dated 9/13/02.

Remarks:

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm *or* Individual name	Theodore A. Gottlieb NORRIS McLAUGHLIN & MARCUS, P.A.	
Signature		Reg. No. 42,597
Date	October 1, 2002	

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to : Hon. Assistant Commissioner of Patents, Washington, D.C. 20231.

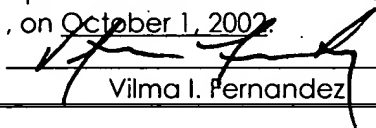| Typed or printed name	Vilma I. Fernandez		
Signature		Date	October 1, 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

SERIAL NO.	09/786,635
APPLICANT	Gerd SCHMITZ et al.,
FILED	May 22, 2001
EXAMINER	Joseph Murphy
ART UNIT	1646
FOR	**ATP BINDING CASSETTE GENES AND PROTEIN FOR DIAGNOSIS AND TREATMENT OF LIPID DISORDERS AND INFLAMMATORY DISEASES**

Hon. Assistant Commissioner of Patents
c/o Examiner Joseph Murphy
Crystal Mall 1
7th Floor Reception
1911 South Clark Street
Arlington, VA 22202

October 13, 2002

RESPONSE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Sir:

This communication is in response to the Notice to Comply mailed on September 13, 2002.

CONDITIONAL PETITION FOR EXTENSION OF TIME

If any extension of time for this response is required, Applicants

request that this be considered a petition therefore. Please charge the required fee

to Deposit Account No. 14-1263.

ADDITIONAL FEES

Please charge any further insufficiency of fees, or credit any excess to

Deposit Account No. 14-1263.

REMARKS

Enclosed herewith, is a copy of the amended Sequence Listing on a computer readable diskette.

The undersigned affirms that the amended sequence listing in the accompanying diskette does not comprise new matter. In addition, the only changes are those required in the NOTICE, a copy of which is attached.

The nucleotide and amino acid sequences disclosed in the accompanying diskette are believed to be identical to those originally filed.

Respectfully submitted,
NORRIS, MCLAUGHLIN & MARCUS

Theodore A. Gottlieb, Ph.D.
Reg. No. 42,597
220 East 42nd Street
New York, NY 10017
telephone (646) 487-5675
facsimile (212) 808-0844

UNITED STATES PATENT AND TRADEMARK OFFICE

Bayer 10131-KBB

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/786,635	05/22/2001	Gerd Schmitz	Bayer 10,131-KGB	3503

7590   09/13/2002

Norris McLaughlin & Marcus
30th Floor
220 East 42nd Street
New York, NY   10017

Sequence ded 10-13-02

EXAMINER
MURPHY, JOSEPH F

ART UNIT	PAPER NUMBER
1646	

DATE MAILED: 09/13/2002   6

Please find below and/or attached an Office communication concerning this application or proceeding.

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

Address: ASSISTANT COMMISSIONER FOR PATENTS
Washington, D.C. 20231

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

EXAMINER

ART UNIT	PAPER

6

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Sequence Rules

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice to Comply with Sequence Rules and Raw Sequence Listing Error Report.

Applicant is given ONE MONTH from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Advisory Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Joseph F. Murphy whose telephone number is 703-305-7245. The examiner can normally be reached on M-F 7:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler can be reached on 703-308-6564. The fax phone numbers for the organization where this application or proceeding is assigned are 703-305-3014 for regular communications and 703-308-0294 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Joseph F. Murphy, Ph. D.
Patent Examiner
Art Unit 1646

Application No. 09 178662

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
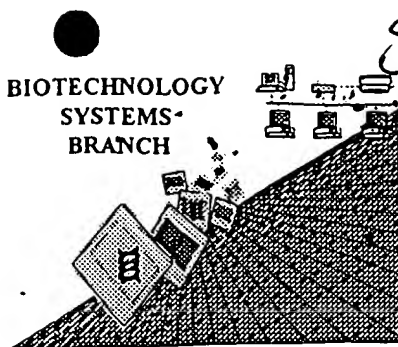For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Applicant copy

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/786635___

Source: ___PCT 09___

Date Processed by STIC: ___11/14/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/786635

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 0; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5ᵗ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length.

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequen-
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MII – Biotechnology Systems Branch – 08/21/2001

PCT09

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/786,635   TIME: 14:04:22

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Output Set: N:\CRF3\11142001\I786635.raw

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 5 <120> TITLE OF INVENTION: ATP binding cassette genes and proteins for diagnosis
 6       and treatment of lipid disorders and inflammatory
 7       diseases
 9 <130> FILE REFERENCE: ATP binding cassette genes and protein
11 <140> CURRENT APPLICATION NUMBER: US/09/786,635  DK
12 <141> CURRENT FILING DATE: 2001-03-07
14 <150> PRIOR APPLICATION NUMBER: 101706
15 <151> PRIOR FILING DATE: 1998-09-25
17 <160> NUMBER OF SEQ ID NOS: 54
19 <170> SOFTWARE: PatentIn Ver. 2.0
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      11/14/01

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/786,635   TIME: 14:04:22

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PATENT APPLICATION: US/09/786,635   TIME: 14:04:22

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116 ctacttttgc tgtatgggtg gtcaatcaca cctctcatgt acccagcctc ctttgtgttc 5220
117 aagatcccca gcacagccta tgtggtgctc accagcgtga acctcttcat tggcattaat 5280
118 ggcagcgtgg ccacctttgt gctggagctg ttcaccgaca ataagctgaa taatatcaat 5340
119 gatatcctga agtccgtgtt cttgatcttc ccacattttt gcctgggacg agggctcatc 5400
120 gacatggtga aaaaccaggc aatggctgat gccctggaaa ggtttggggga gaatcgcttt 5460
121 gtgtcaccat tatcttggga cttggtggga cgaaacctct tcgccatggc cgtggaaggg 5520
122 gtggtgttct tcctcattac tgttctgatc cagtacagat tcttcatcag gcccagacct 5580
123 gtaaatgcaa agctatctcc tctgaatgat gaagatgaag atgtgaggcg ggaaagacag 5640
124 agaattcttg atggtggagg ccagaatgac atcttagaaa tcaaggagtt gacgaagata 5700
125 tatagaagga agcggaagcc tgctgttgac aggatttgcg tgggcattcc tcctggtgag 5760
126 tgctttgggc tcctgggagt taatgggggct ggaaaatcat caactttcaa gatgttaaca 5820
127 ggagatacca ctgttaccag aggagatgct ttccttaaca gaaatagtat cttatcaaac 5880
128 atccatgaag tacatcagaa catgggctac tgccctcagt ttgatgccat cacagagctg 5940
129 ttgactggga gagaacacgt ggagttcttt gcccttttga gaggagtccc agagaaagaa 6000
130 gttggcaagg ttggtgagtg ggcgattcgg aaactgggcc tcgtgaagta tggagaaaaa 6060
131 tatgctggta actatagtgg aggcaacaaa cgcaagctct ctacagccat ggctttgatc 6120
132 ggcgggcctc ctgtggtgtt tctggatgaa cccaccacag gcatggatcc caaagcccgg 6180
133 cggttcttgt ggaattgtgc cctaagtgtt gtcaaggagg ggagatcagt agtgcttaca 6240
134 tctcatagta tggaagaatg tgaagctctt tgcactagga tggcaatcat ggtcaatgga 6300
135 aggttcaggt gccttggcag tgtccagcat ctaaaaaata ggtttggaga tggttataca 6360
136 atagttgtac gaatagcagg gtccaacccg gacctgaagc ctgtccagga tttctttgga 6420
137 cttgcatttc ctggaagtgt tccaaaagag aaacaccgga acatgctaca ataccagctt 6480
138 ccatcttcat tatcttctct ggccaggata ttcagcatcc tctcccagag caaaaagcga 6540
139 ctccacatag aagactactc tgtttctcag acaacacttg accaagtatt tgtgaacttt 6600
140 gccaaggacc aaagtgatga tgaccactta aaagacctct cattacacaa aaaccagaca 6660
141 gtagtggacg ttgcagttct cacatctttt ctacaggatg agaaagtgaa agaaagctat 6720
142 gtatgaagaa tcctgttcat acggggtggc tgaaagtaaa gagggactag actttccttt 6780
143 gcaccatgtg aagtgttgtg gagaaaagag ccagaagttg atgtgggaag aagtaaactg 6840
144 gatactgtac tgatactatt caatgcaatg caattcaatg                        6880
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 2201
148 <212> TYPE: PRT
149 <213> ORGANISM: Human
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Peptide sequence of ABCA1 (ABC1)
154 <400> SEQUENCE: 2
155 Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn
156  1               5                  10                  15
158 Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly
159                 20                  25                  30
161 Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/786,635

Input Set : A:\Lea33298.app
Output Set: N:\CRF3\11142001\I786635.raw

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162           35                    40                    45
164 Ala Arg Arg Leu Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp
165        50                    55                    60
167 Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser
168 65                    70                    75                    80
170 Asn Leu Lys Leu Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly
171                   85                    90                    95
173 Phe Leu Tyr His Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met
174           100                   105                   110
176 Leu Arg Ala Asp Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln
177        115                   120                   125
179 Leu His Leu Thr Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile
180        130                   135                   140
182 Gln Leu Gly Asp Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Arg Glu
183 145                   150                   155                   160
185 Lys Leu Ala Ala Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu
186           165                   170                   175
188 Lys Pro Ile Leu Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys
189           180                   185                   190
191 Glu Leu Ala Glu Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu
192           195                   200                   205
194 Ala Gln Glu Leu Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu
195        210                   215                   220
197 Val Met Phe Leu Thr Asn Val Asn Ser Ser Ser Ser Ser Thr Gln Ile
198 225                   230                   235                   240
200 Tyr Gln Ala Val Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Gly
201           245                   250                   255
203 Leu Lys Ile Lys Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala
204           260                   265                   270
206 Leu Phe Gly Gly Asn Gly Thr Glu Glu Asp Ala Glu Thr Phe Tyr Asp
207        275                   280                   285
209 Asn Ser Thr Thr Pro Tyr Cys Asn Asp Leu Met Lys Asn Leu Glu Ser
210        290                   295                   300
212 Ser Pro Leu Ser Arg Ile Ile Trp Lys Ala Leu Lys Pro Leu Leu Val
213 305                   310                   315                   320
215 Gly Lys Ile Leu Tyr Thr Pro Asp Thr Pro Ala Thr Arg Gln Val Met
216           325                   330                   335
218 Ala Glu Val Asn Lys Thr Phe Gln Glu Leu Ala Val Phe His Asp Leu
219           340                   345                   350
221 Glu Gly Met Trp Glu Glu Leu Ser Pro Lys Ile Trp Thr Phe Met Glu
222        355                   360                   365
224 Asn Ser Gln Glu Met Asp Leu Val Arg Met Leu Leu Asp Ser Arg Asp
225        370                   375                   380
227 Asn Asp His Phe Trp Glu Gln Gln Leu Asp Gly Leu Asp Trp Thr Ala
228 385                   390                   395                   400
230 Gln Asp Ile Val Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser
231           405                   410                   415
233 Ser Asn Gly Ser Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu Thr Asn
234           420                   425                   430
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/786,635

DATE: 11/14/2001
TIME: 14:04:22

Input Set : A:\Lea33298.app
Output Set: N:\CRF3\11142001\I786635.raw

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236 Gln Ala Ile Arg Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn
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239 Lys Leu Glu Pro Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met
240     450             455             460
242 Glu Leu Leu Asp Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly
243 465             470             475             480
245 Ile Thr Pro Gly Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile
246             485             490             495
248 Arg Met Asp Ile Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly
249         500             505             510
251 Tyr Trp Asp Pro Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Arg Tyr
252     515             520             525
254 Val Trp Gly Gly Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile
255     530             535             540
257 Ile Arg Val Leu Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln
258 545             550             555             560
260 Gln Met Pro Tyr Pro Cys Tyr Val Asp Asp Ile Phe Leu Arg Val Met
261             565             570             575
263 Ser Arg Ser Met Pro Leu Phe Met Thr Leu Ala Trp Ile Tyr Ser Val
264             580             585             590
266 Ala Val Ile Ile Lys Gly Ile Val Tyr Glu Lys Glu Ala Arg Leu Lys
267         595             600             605
269 Glu Thr Met Arg Ile Met Gly Leu Asp Asn Ser Ile Leu Trp Phe Ser
270     610             615             620
272 Trp Phe Ile Ser Ser Leu Ile Pro Leu Leu Val Ser Ala Gly Leu Leu
273 625             630             635             640
275 Val Val Ile Leu Lys Leu Gly Asn Leu Leu Pro Tyr Ser Asp Pro Ser
276             645             650             655
278 Val Val Phe Val Phe Leu Ser Val Phe Ala Val Val Thr Ile Leu Gln
279             660             665             670
281 Cys Phe Leu Ile Ser Thr Leu Phe Ser Arg Ala Asn Leu Ala Ala Ala
282     675             680             685
284 Cys Gly Gly Ile Ile Tyr Phe Thr Leu Tyr Leu Pro Tyr Val Leu Cys
285     690             695             700
287 Val Ala Trp Gln Asp Tyr Val Gly Phe Thr Leu Lys Ile Phe Ala Ser
288 705             710             715             720
290 Leu Leu Ser Pro Val Ala Phe Gly Phe Gly Cys Glu Tyr Phe Ala Leu
291             725             730             735
293 Phe Glu Glu Gln Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser
294             740             745             750
296 Pro Val Glu Glu Asp Gly Phe Asn Leu Thr Thr Ser Val Ser Met Met
297         755             760             765
299 Leu Phe Asp Thr Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala
300     770             775             780
302 Val Phe Pro Gly Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys
303 785             790             795             800
305 Thr Lys Ser Tyr Trp Phe Gly Glu Glu Ser Asp Glu Lys Ser His Pro
306             805             810             815
308 Gly Ser Asn Gln Lys Arg Ile Ser Glu Ile Cys Met Glu Glu Glu Pro
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09/786635

<210> 3
<211> 1130
<212> DNA
<213> Human

<220>
<223> human cDNA of ABCB9

<400> 3
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ggaaccccccc agtcctcatc ctggatgaag ccaccagcgc tttggatgcc gagagcgagt 180
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cggatttttc cgtctctccc tcttgccagc tctgtgagtc tggccagggc gggtagggag 780
cgtggagggc atctgtctgc caattgcccg ctgccaatct aagccagtct cactgtgacc 840
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```

Unknowns must be enumerated in fields 221, 222 and 223

Global

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/786,635

DATE: 11/14/2001
TIME: 14:04:23

Input Set : A:\Lea33298.app
Output Set: N:\CRF3\11142001\I786635.raw

```
L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:579 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:579 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:584 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:588 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:588 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:596 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:596 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:623 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:623 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1213 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1213 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1577 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1577 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1625 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1625 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1720 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1720 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1986 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
```

VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: US/09/786,635   TIME: 14:04:23

Input Set : A:\Lea33298.app
Output Set: N:\CRF3\11142001\I786635.raw

```
L:1986 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1988 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1988 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1990 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1990 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2013 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:2013 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:2013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2014 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:2014 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:2014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2289 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:2289 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:2289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2291 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:2291 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
```